

Re-req

See p.5 #4
ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/300,482

DATE: 09/15/2000
TIME: 10:50:56

Input Set : A:\phosphoglucseq.rpt
Output Set: N:\CRF3\09152000\I300482.raw

2 <110> APPLICANT: Cheikh, Nordine
3 Liu, Jingdong
4 Peschke, Virginia M.
6 <120> TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
7 Phosphogluconate Pathway
9 <130> FILE REFERENCE: 04983.0031.US01/38-21(15365)B
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/300,482
C--> 11 <141> CURRENT FILING DATE: 1999-04-28
11 <160> NUMBER OF SEQ ID NOS: 699
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 233
15 <212> TYPE: DNA
16 <213> ORGANISM: Zea mays
18 <400> SEQUENCE: 1
20 gtttttgcag ttagtagaat atgttagtgg ctcctatgtat agggtggaaag gatttggat 60
22 atggatgag gcaatctcg atgtatgagac ttcaaaaaac aatgactcg gaaatctaccg 120
24 cagattttt tattttggat tgcctccatc agtctaccca tcagttatgcg agatgataag 180
26 atcatattgc atgagtccat cttcacacac cgggttggaca agggtttatttggat 233
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 180
31 <212> TYPE: DNA
32 <213> ORGANISM: Zea mays
34 <400> SEQUENCE: 2
36 tcgttcggca gcagcaacga ggtgctggat gggacgccga cgggagatgg ggcacccggg 60
38 caggggcage ggggagggag caccgtcage atcacggtcg tcggcgccctc cggcgcaccc 120
40 gccaagaaga agatcttccc ggcctcttc gccttggatc acgagggtcg gctccggag 180
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 137
45 <212> TYPE: DNA
46 <213> ORGANISM: Zea mays
48 <400> SEQUENCE: 3
50 cacagatctt gatagggcca ctaatgagct tggatacgat gtgcacccgg atgaagcaat 60
52 ttacccaaag attacaaca agattctgg ttcggatcgatc cgactagata ggagtaactt 120
54 gaatctccat tatggcg 137
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 263
59 <212> TYPE: DNA
60 <213> ORGANISM: Glycine max
62 <223> OTHER INFORMATION: unsure at all n locations
W--> 63 <400> SEQUENCE: 4
65 gaagcacctt tggatgttgc gtcatgttgc tcaagcgttg ctcagaccca gaaggatgg 60
67 aatccgataa tattttggaa gccatttggc ttgtatgcac tttcttccca taggtctgaca 120
W--> 69 caaatatcttc ttcaaaactt tcaggaaaag caaatatata gaattganca tctacttagga 180
W--> 71 aggaatcnca gthaaaaatcc tncagggttta agggtttcaa annnagnttt tgagccacct 240
W--> 73 tngagnnnga ctnnnnnnnga nna 263
76 <210> SEQ ID NO: 5.
77 <211> LENGTH: 259

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163 ctgcactttt ccacctatac ctggcaggga ttcttaccac cagatga 287
166 <210> SEQ ID NO: 10
167 <211> LENGTH: 251
168 <212> TYPE: DNA
169 <213> ORGANISM: Glycine max
171 <223> OTHER INFORMATION: unsure at all n locations
W--> 172 <400> SEQUENCE: 10
W--> 174 cttttctctc tctgaactc gaagcnaaac aacattacca gagtggttct agtaattcag 60
176 tgctgtaga agatggaaac tagtgaatgg catabcgac gaagatctag cttcggctct 120
178 gaatccccct agcaagagag gcagggaaatg tgcctgaaac tgggtcactc tctattgtgg 180
180 tgcttgggtc ttcttgggtat cttgtctaaaga agaagacatt tcctgcactt ttccacat 240
W--> 182 acctgngnta c 251
185 <210> SEQ ID NO: 11
186 <211> LENGTH: 193
187 <212> TYPE: DNA
188 <213> ORGANISM: Glycine max
190 <223> OTHER INFORMATION: unsure at all n locations
W--> 191 <400> SEQUENCE: 11
193 gttttagtca actctgtttc acttggtaat ttagtggttc tagtaatccg gtgtgtctag 60
195 aggatggaa ctatgtatcgatc gcatatcgag cgaagatcta gcttcggcac tgaatcccc 120
W--> 197 ttagcaagat atgcaggaaat tgcctgaaactcgggtcactc tctctattgt tgcgttggc 180
199 gcttctgggg atc 193
202 <210> SEQ ID NO: 12
203 <211> LENGTH: 318
204 <212> TYPE: DNA
205 <213> ORGANISM: Zea mays
207 <223> OTHER INFORMATION: unsure at all n locations
W--> 208 <400> SEQUENCE: 12
W--> 210 gcgaggccaag agcgtggaga ntngatggaa ctttaaccc tcgagagctt ccaggatntg 60
212 gaaggccgc tgattatcc gtgcgaggtt cttgtatagg atcaagagcg cgtacgacag 120
214 gaatctcgat ctcggccatg ggcggccat ttgaggatt ggttggatg agcaggatg 180
216 ttttctgtttt tgggtgatattt ctctctgtgg ttatctttc ctttactat ttatcttt 240
218 atgcttcttag atccaagtcg agtacttcga ataatgtctgt actgtatggt tggcaagtg 300
220 agaaacatgt gtatctc 318
223 <210> SEQ ID NO: 13
224 <211> LENGTH: 467
225 <212> TYPE: DNA
226 <213> ORGANISM: Zea mays
228 <223> OTHER INFORMATION: unsure at all n locations
W--> 229 <400> SEQUENCE: 13
231 ggccaaagc ggggagaaag gctgggggtt caacccgttc gtccttcagc ccgtctagga 60
233 acctcgatc caaggacgccc tgcgtatcgat gaggccgcac cgacatcgcc gcccgtct 120
235 gacccgttca cttccctgtc ctttcatcc cggcttgc aaggacattt tccaccagg 180
W--> 237 agccatcgcc atgcgtcgcc ttgtatgccaa agatgtcgcc cgtgtatctt atcaagaagc 240
239 tcaggagtc gcccgttgc cactggaga acacctgggt cagtcactg ttggtgagct 300
W--> 241 taccgaccga cttggaaacgc tgcgtatgcctt nggaaatcaa ctgcatactcg gcataactcg 360
W--> 243 ttccgttggt gaaccatttt nacaaaantt ncccgatnca ncttngcca agtacgttac 420
W--> 245 acaaangggc cacttttaa gggccttta anaaancncc tttnnmng 467
248 <210> SEQ ID NO: 14

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249 <211> LENGTH: 410
 250 <212> TYPE: DNA
 251 <213> ORGANISM: Zea mays
 253 <223> OTHER INFORMATION: unsure at all n locations
 W--> 254 <400> SEQUENCE: 14
 256 cccacgcgtc cgccgtcatg gggcagaacc ttgcctcaa cattgcagag aaagggttcc 60
 258 ccatctctgt gtacaacagg acaaacctcca aagggtggacga gaccgtgcag cgtgccaagg 120
 260 cagaaggaaa ccttcccggtc tacggcttcc atgaccggcgc gtcccttggta aagtccattc 180
 262 aagaaggccaccc ggtgtgtatc atgtctgtca aaggccggcgc gccagttgac cagaccatcg 240
 264 cgacgctcgc agtctacttg gaggcaggccg actgcatcat cgtatgggggg aacgagttgt 300
 W--> 266 acgagaacac ggagaggagg gagaaggcca tggaggagcg cggcctnctg tatcttggca 360
 268 tgggtgtctc tggaggaaag gagggtgccc gcaacggccc gtcccttgatg 410
 271 <210> SEQ ID NO: 15
 272 <211> LENGTH: 449
 273 <212> TYPE: DNA
 274 <213> ORGANISM: Zea mays
 276 <400> SEQUENCE: 15
 278 cccacgcgtc cgccacacgcg ttccgggtgt ttgacgggtc tggcatgc aattcaactc 60
 280 cgcacatcgca tcggcagcgc gcacgttca tagtgttagga ggagatggcg ctcacaagaa 120
 282 tcggcttgc tggccttgcg gtcatggggc aagaaccttc cctcaacattt gcagagaaag 180
 284 gtttcccat ctctgtgtac aacaggacaa ccttcagggt ggacgagacc gtgcagctg 240
 286 ccaaggcaga aggaacacctt cccgtctacg gtttccatga ccccgctcc tttgtgaagt 300
 288 catttcagaa gccacgggtg gtgtatcatgc tcgtcaaggc cggcgcgcctt gttgaccaga 360
 290 ccatcgcgac gctcgcagct cacttggacg aaggccgactg catcatcgat aggggaaacg 420
 292 agtggtagca gaaacacggag aggagggg 449
 295 <210> SEQ ID NO: 16
 296 <211> LENGTH: 410
 297 <212> TYPE: DNA
 298 <213> ORGANISM: Zea mays
 300 <400> SEQUENCE: 16
 302 ggcacttcc ctgcctgtt ggcgtatcaa gcccgggggg agggaaaggcc gatggtaagt 60
 304 gaaagagagt aggtggacgg acgggtgtgg catcgccaaat tcaactccgc atctgcatcg 120
 306 gcagcgcgc agctccatag tggtaggagga gatggcgcgc acaagaatcg gtcttgcgg 180
 308 ccttgcgtc atggggcaga accttgcctt caacatttgc gagaagggt tcccatctc 240
 310 tggtaacaac aggacaaccc ccaagggtga cggacccgtg cagcgtgcca aggccagaagg 300
 312 aaaccttcc gtcatacggt tccatgaccc cggccctttt gttgaactcca ttcagaagcc 360
 314 acgggtggtg atcatgtcg tcaaggccgg cggcccgatg gaccagacca 410
 317 <210> SEQ ID NO: 17
 318 <211> LENGTH: 409
 319 <212> TYPE: DNA
 320 <213> ORGANISM: Zea mays
 322 <400> SEQUENCE: 17
 324 aggtggccgg acgggtggtg catcgccaaat tcaactccgc atctgaatcg gcactccggca 60
 326 gcgcggcaggc tccatgtgtt agggaggaga gatggcgcgc acaagaatcg gtcttgcgg 120
 328 ctttgcgtc atggggcaga accttgcctt caacatttgc gagaagggt tcccatctc 180
 330 tggtaacaac aggacaaccc ccaagggtga cggacccgtg cagcgtgcca aggccagaagg 240
 332 aaaccttcc gtcatacggt tccatgaccc cggccctttt gttgaactcca ttcagaagcc 300
 334 acgggtggtg atcatgtcg tcaaggccgg cggcccgatg gaccagacca tcgcgacgt 360
 336 cgcagctcac ttggagcagg gcgactcgat catcgatgg gggaaacgag 409

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Input Set : A:\phosphoglucseq.rpt
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339 <210> SEQ ID NO: 18
340 <211> LENGTH: 420
341 <212> TYPE: DNA
342 <213> ORGANISM: Zea mays
344 <400> SEQUENCE: 18
346 ggtggacgga cgtgtctggc atcgccaaatt caacttcgca tctgcattcg cagcgcgcca 60
348 gctccatagg aggagatggc gtcacaaga atcggcttgc ctggcccttc ggtcatgggg 120
350 cagaacccatgg ccttcaacat tgcagaaaaa gggttccca tctctgttca caacaggaca 180
352 accttcaagg tggacgagac cgtgcagcgt gccaaggcag aaggaaacct tcccgctac 240
354 ggcttccatg accccgcgtc ctttgtaag tccattcaga agccacgggt ggtgatcatg 300
356 ctcgtcaagg cggcgcgc accatcgca cgctcgacg tcacttggag 360
358 caggcgcact gcatcatcgta tagggggAAC gagggttacg aggacacggaa gaggaggag 420
361 <210> SEQ ID NO: 19
362 <211> LENGTH: 403
363 <212> TYPE: DNA
364 <213> ORGANISM: Zea mays
366 <400> SEQUENCE: 19
368 agcggacgcg tggggacgg acgggtctgg catcgccaaat tcaactccgc atctgcattcg 60
370 gcagcgcgc agctccatg ttagggagga gatggcgctc acaagaatcg gtcttgcgg 120
372 ccttgcgtc atggggcaga accttgcctt caacatttgcg gagaagggt tccccatctc 180
374 tggatacaac aggacaaaccc tcaagggttgc cggacccgtg cagcgtgcgca aggccagaagg 240
376 aaaccttccc gtctacggct tccatgcacc cggcgttgc tgcgttgc ttcagaagcc 300
378 acgggtgggt atcatgcctcg tcaaggcggc cggccaggta gaccgacca tccgcacgt 360
380 cgcagctcac ttggacggc gggactgcattcatcgatggg ggg 403
383 <210> SEQ ID NO: 20
384 <211> LENGTH: 433
385 <212> TYPE: DNA
386 <213> ORGANISM: Zea mays
388 <400> SEQUENCE: 20
390 ggcaacttcc ctgcgttgcattt ggcgattttat aecgggtgggg gagggaaggc cgtggtcag 60
392 gggaaagagag tagtggacg gacgggtgt gcatecgccaa ttcaacttgc catttgcattcg 120
394 ggcacgcgc cagctccatgg ggaggagatg gggctcaaa gaatcggttct tgcgttgcctt 180
396 gcggtcatgg ggcagaaccc tccctcaac atttgcagaga aagggttccc catttctgt 240
398 tacaacacgg caacccctccatgg ggcggacgg accgtgcgcg tgcgttgc tggccaggc agaaggaaac 300
400 cttccgttgc acggtttcca tgacccgcg tcccttgc tgcgttgc tgcgttgc tggccaggc 360
402 gtgggtatca tgctgtcaa ggcggcgcg ccagttgacc agaccatcgca gacgctcgca 420
404 gctcaacttgg agc 433
407 <210> SEQ ID NO: 21
408 <211> LENGTH: 209
409 <212> TYPE: DNA
410 <213> ORGANISM: Zea mays
412 <223> OTHER INFORMATION: unsure at all n locations
W--> 413 <400> SEQUENCE: 21
W--> 415 gcatctgcattt cggcagcgcg ncagnnnat aggaggagat ggcgctcaca agaattcgtn 60
W--> 417 ttgttgcgtt tgcgttgcgtt gggcagaacc ttgcgttgcgtt catttgcagaa aagggnnnn 120
W--> 419 ccataatgtgtt gnacaaacagg acaacccgtca aggttngacna gaccgttgcg ngnncnagg 180
W--> 421 cagaangana ctttangntt tannnattt 209
424 <210> SEQ ID NO: 22
425 <211> LENGTH: 271

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Input Set : A:\phosphoglucseq.rpt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:63 M:283 W: Missing Blank Line separator, <400> field identifier
L:69 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:69 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:69 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:69 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:71 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:71 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:71 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:73 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:73 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:73 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:82 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:84 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:84 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:84 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:86 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:86 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:86 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:88 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:88 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:88 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:92 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:92 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:92 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:103 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:103 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:105 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:105 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:105 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:107 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:109 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:109 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:111 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6

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L:111 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:111 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:120 M:283 W: Missing Blank Line separator, <400> field identifier
L:122 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:122 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:122 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:122 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:124 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:124 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:124 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:126 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:126 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:159 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:159 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:159 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:172 M:283 W: Missing Blank Line separator, <400> field identifier
L:174 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:191 M:283 W: Missing Blank Line separator, <400> field identifier
L:197 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:208 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:229 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:254 M:283 W: Missing Blank Line separator, <400> field identifier
L:266 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:413 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
M:340 Repeated in SeqNo=21
L:430 M:283 W: Missing Blank Line separator, <400> field identifier
L:432 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:465 M:283 W: Missing Blank Line separator, <400> field identifier
L:471 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
M:340 Repeated in SeqNo=24
L:600 M:283 W: Missing Blank Line separator, <400> field identifier
L:608 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
M:340 Repeated in SeqNo=32
L:685 M:283 W: Missing Blank Line separator, <400> field identifier
L:691 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
L:756 M:283 W: Missing Blank Line separator, <400> field identifier
L:758 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:41
M:340 Repeated in SeqNo=41
L:1105 M:283 W: Missing Blank Line separator, <400> field identifier

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Input Set : A:\phosphoglucseq.rpt
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L:1113 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61
 L:1142 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1148 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
 M:340 Repeated in SeqNo=63
 L:1197 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1199 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:66
 M:340 Repeated in SeqNo=66
 L:1320 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1322 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:73
 M:340 Repeated in SeqNo=73
 L:1375 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1377 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:76
 M:340 Repeated in SeqNo=76
 L:1820 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1824 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101
 L:1861 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1875 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103
 L:1916 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1918 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:106
 M:340 Repeated in SeqNo=106
 L:1935 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1939 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:107
 M:340 Repeated in SeqNo=107
 L:2458 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2464 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:138
 M:340 Repeated in SeqNo=138
 L:2479 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2489 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:139
 M:340 Repeated in SeqNo=139
 L:2500 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2506 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:140
 L:2611 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2613 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:146
 M:340 Repeated in SeqNo=146
 L:2870 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2891 M:283 W: Missing Blank Line separator, <400> field identifier
 L:2912 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3097 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3134 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3721 M:283 W: Missing Blank Line separator, <400> field identifier
 L:3806 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4131 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4300 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4357 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4446 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4631 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4676 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4739 M:283 W: Missing Blank Line separator, <400> field identifier
 L:4758 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/300,482

DATE: 09/15/2000

TIME: 10:50:57

Input Set : A:\phosphoglucseq.rpt

Output Set: N:\CRF3\09152000\I300482.raw

L:4795 M:283 W: Missing Blank Line separator, <400> field identifier
L:4900 M:283 W: Missing Blank Line separator, <400> field identifier
L:4919 M:283 W: Missing Blank Line separator, <400> field identifier
L:4956 M:283 W: Missing Blank Line separator, <400> field identifier
L:4975 M:283 W: Missing Blank Line separator, <400> field identifier
L:5210 M:283 W: Missing Blank Line separator, <400> field identifier